David Torrents

List of Publications by Year in Descending Order

83 papers	27,244 citations	42 h-index	95 g-index
95 ext. papers	32,491 ext. citations	19.9 avg, IF	7.25 L-index

#	Paper	IF	Citations
83	In Search of Complex Disease Risk through Genome Wide Association Studies. *Mathematics*, **2021**, 9, 3083	2.3	
82	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. *Cell Genomics*, **2021**, 1, 100029-100029		20
81	Recessive Genome-wide Meta-analysis Illuminates Genetic Architecture of Type 2 Diabetes. *Diabetes*, **2021**,	0.9	0
80	TIGER: The gene expression regulatory variation landscape of human pancreatic islets. *Cell Reports*, **2021**, 37, 109807	10.6	5
79	The impact of non-additive genetic associations on age-related complex diseases. *Nature Communications*, **2021**, 12, 2436	17.4	10
78	Polymorphic Inversions Underlie the Shared Genetic Susceptibility of Obesity-Related Diseases. *American Journal of Human Genetics*, **2020**, 106, 846-858	11	3
77	Genomic and epigenomic insights into the origin, pathogenesis, and clinical behavior of mantle cell lymphoma subtypes. *Blood*, **2020**, 136, 1419-1432	2.2	53
76	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
75	Extrachromosomal circular DNA drives oncogenic genome remodeling in neuroblastoma. *Nature Genetics*, **2020**, 52, 29-34	36.3	70
74	Enhancer hijacking determines extrachromosomal circular MYCN amplicon architecture in neuroblastoma. *Nature Communications*, **2020**, 11, 5823	17.4	34
73	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nature Communications*, **2020**, 11, 4748	17.4	10
72	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. *Nature Genetics*, **2019**, 51, 804-814	36.3	181
71	Insight into genetic predisposition to chronic lymphocytic leukemia from integrative epigenomics. *Nature Communications*, **2019**, 10, 3615	17.4	19
70	Human pancreatic islet three-dimensional chromatin architecture provides insights into the genetics of type 2 diabetes. *Nature Genetics*, **2019**, 51, 1137-1148	36.3	111
69	and hijack immunoglobulin light-chain enhancers in cyclin D1 mantle cell lymphoma. *Blood*, **2019**, 133, 940-951	2.2	48
68	Genomic profiling in advanced stage non-small-cell lung cancer patients with platinum-based chemotherapy identifies germline variants with prognostic value in SMYD2. *Cancer Treatment and Research Communications*, **2018**, 15, 21-31	2	8
67	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. *Nature Communications*, **2018**, 9, 321	17.4	50

66	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. *Nature Genetics*, **2018**, 50, 1072-1080	36.3	52
65	Genome-wide association study meta-analysis identifies five new loci for systemic lupus erythematosus. *Arthritis Research and Therapy*, **2018**, 20, 100	5.7	47
64	A cancer-associated polymorphism in ESCRT-III disrupts the abscission checkpoint and promotes genome instability. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E8900-E8908	11.5	28
63	Multitrait genome association analysis identifies new susceptibility genes for human anthropometric variation in the GCAT cohort. *Journal of Medical Genetics*, **2018**, 55, 765-778	5.8	12
62	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. *Nature Medicine*, **2018**, 24, 868-880	50.5	103
61	A kidney-disease gene panel allows a comprehensive genetic diagnosis of cystic and glomerular inherited kidney diseases. *Kidney International*, **2018**, 94, 363-371	9.9	57
60	PGBD5 promotes site-specific oncogenic mutations in human tumors. *Nature Genetics*, **2017**, 49, 1005-1014	36.3	40
59	Dysregulation of Placental miRNA in Maternal Obesity Is Associated With Pre- and Postnatal Growth. *Journal of Clinical Endocrinology and Metabolism*, **2017**, 102, 2584-2594	5.6	45
58	Metformin alters the gut microbiome of individuals with treatment-naive type 2 diabetes, contributing to the therapeutic effects of the drug. *Nature Medicine*, **2017**, 23, 850-858	50.5	732
57	A Loss-of-Function Splice Acceptor Variant in Is Protective for Type 2 Diabetes. *Diabetes*, **2017**, 66, 2903-2914	9.4	32
56	The BLUEPRINT Data Analysis Portal. *Cell Systems*, **2016**, 3, 491-495.e5	10.6	71
55	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149	56.2	232
54	Tuning fresh: radiation through rewiring of central metabolism in streamlined bacteria. *ISME Journal*, **2016**, 10, 1902-14	11.9	31
53	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. *Genome Biology*, **2016**, 17, 11	18.3	141
52	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	36.4	266
51	Non-coding recurrent mutations in chronic lymphocytic leukaemia. *Nature*, **2015**, 526, 519-24	50.4	565
50	Altered Circulating miRNA Expression Profile in Pregestational and Gestational Obesity. *Journal of Clinical Endocrinology and Metabolism*, **2015**, 100, E1446-56	5.6	68
49	Surgery-Induced Weight Loss Is Associated With the Downregulation of Genes Targeted by MicroRNAs in Adipose Tissue. *Journal of Clinical Endocrinology and Metabolism*, **2015**, 100, E1467-76	5.6	35

48	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. *Nature Communications*, **2015**, 6, 10001	17.4	199
47	A genome-wide association study identifies CDHR3 as a susceptibility locus for early childhood asthma with severe exacerbations. *Nature Genetics*, **2014**, 46, 51-5	36.3	376
46	Comprehensive characterization of complex structural variations in cancer by directly comparing genome sequence reads. *Nature Biotechnology*, **2014**, 32, 1106-12	44.5	62
45	Somatic signature of brain-specific single nucleotide variations in sporadic Alzheimer's disease. *Journal of Alzheimer's Disease*, **2014**, 42, 1357-82	4.3	31
44	Genomics of ecological adaptation in cactophilic Drosophila. *Genome Biology and Evolution*, **2014**, 7, 349-66	3.9	38
43	Adaptation to environmental factors shapes the organization of regulatory regions in microbial communities. *BMC Genomics*, **2014**, 15, 877	4.5	13
42	Unravelling the hidden DNA structural/physical code provides novel insights on promoter location. *Nucleic Acids Research*, **2013**, 41, 7220-30	20.1	11
41	Common genetic variants of surfactant protein-D (SP-D) are associated with type 2 diabetes. *PLoS ONE*, **2013**, 8, e60468	3.7	12
40	Impact of methylation on the physical properties of DNA. *Biophysical Journal*, **2012**, 102, 2140-8	2.9	89
39	The tomato genome sequence provides insights into fleshy fruit evolution. *Nature*, **2012**, 485, 635-41	50.4	2138
38	BLUEPRINT to decode the epigenetic signature written in blood. *Nature Biotechnology*, **2012**, 30, 224-6	44.5	261
37	Identification of novel type 2 diabetes candidate genes involved in the crosstalk between the mitochondrial and the insulin signaling systems. *PLoS Genetics*, **2012**, 8, e1003046	6	17
36	ReLA, a local alignment search tool for the identification of distal and proximal gene regulatory regions and their conserved transcription factor binding sites. *Bioinformatics*, **2012**, 28, 763-70	7.2	11
35	Enterotypes of the human gut microbiome. *Nature*, **2011**, 473, 174-80	50.4	4240
34	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. *Nature* , **2011**, 475, 101-5	50.4	1206
33	Selective maintenance of Drosophila tandemly arranged duplicated genes during evolution. *Genome Biology*, **2008**, 9, R176	18.3	10
32	Projection structure of a member of the amino acid/polyamine/organocation transporter superfamily. *Journal of Biological Chemistry*, **2008**, 283, 33240-8	5.4	34
31	DNAlive: a tool for the physical analysis of DNA at the genomic scale. *Bioinformatics*, **2008**, 24, 1731-2	7.2	22

30	Is there selection for the pace of successive inactivation of the arpAT gene in primates?. *Journal of Molecular Evolution*, **2008**, 67, 23-8	3.1	2
29	Functional and structural characterization of the first prokaryotic member of the L-amino acid transporter (LAT) family: a model for APC transporters. *Journal of Biological Chemistry*, **2007**, 282, 13270-81	5.4	35
28	Determining promoter location based on DNA structure first-principles calculations. *Genome Biology*, **2007**, 8, R263	18.3	98
27	Identification and analysis of genes and pseudogenes within duplicated regions in the human and mouse genomes. *PLoS Computational Biology*, **2006**, 2, e76	5	20
26	PAL2NAL: robust conversion of protein sequence alignments into the corresponding codon alignments. *Nucleic Acids Research*, **2006**, 34, W609-12	20.1	1686
25	Protein coding potential of retroviruses and other transposable elements in vertebrate genomes. *Nucleic Acids Research*, **2005**, 33, 946-54	20.1	40
24	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. *Nature*, **2005**, 434, 724-31	50.4	61
23	Initial sequence of the chimpanzee genome and comparison with the human genome. *Nature*, **2005**, 437, 69-87	50.4	1828
22	Identification and functional characterization of a novel low affinity aromatic-preferring amino acid transporter (arpAT). One of the few proteins silenced during primate evolution. *Journal of Biological Chemistry*, **2005**, 280, 19364-72	5.4	21
21	BLAST2GENE: a comprehensive conversion of BLAST output into independent genes and gene fragments. *Bioinformatics*, **2004**, 20, 1968-70	7.2	17
20	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature*, **2004** , 428, 493-521	50.4	1689
19	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature*, **2004**, 432, 695-716	50.4	2143
18	A genome-wide survey of human pseudogenes. *Genome Research*, **2003**, 13, 2559-67	9.7	213
17	The DNA sequence of human chromosome 7. *Nature*, **2003**, 424, 157-64	50.4	202
16	Basolateral LAT-2 has a major role in the transepithelial flux of L-cystine in the renal proximal tubule cell line OK. *Journal of the American Society of Nephrology: JASN*, **2003**, 14, 837-47	12.7	39
15	The human genome: genes, pseudogenes, and variation on chromosome 7. *Cold Spring Harbor Symposia on Quantitative Biology*, **2003**, 68, 13-22	3.9	
14	Initial sequencing and comparative analysis of the mouse genome. *Nature*, **2002**, 420, 520-62	50.4	5376
13	Comparative genome and proteome analysis of Anopheles gambiae and Drosophila melanogaster. *Science*, **2002**, 298, 149-59	33.3	455

12	Sequential amino acid exchange across b(0,+)-like system in chicken brush border jejunum. *Journal of Membrane Biology*, **2001**, 180, 213-20	2.3	37
11	Functional analysis of novel mutations in y(+)LAT-1 amino acid transporter gene causing lysinuric protein intolerance (LPI). *Human Molecular Genetics*, **2000**, 9, 431-8	5.6	56
10	Identification of a membrane protein, LAT-2, that Co-expresses with 4F2 heavy chain, an L-type amino acid transport activity with broad specificity for small and large zwitterionic amino acids. *Journal of Biological Chemistry*, **1999**, 274, 19738-44	5.4	301
9	Non-type I cystinuria caused by mutations in SLC7A9, encoding a subunit (bo,+AT) of rBAT. *Nature Genetics*, **1999**, 23, 52-7	36.3	232
8	Identification of SLC7A7, encoding y+LAT-1, as the lysinuric protein intolerance gene. *Nature Genetics*, **1999**, 21, 293-6	36.3	246
7	Identification and characterization of a membrane protein (y+L amino acid transporter-1) that associates with 4F2hc to encode the amino acid transport activity y+L. A candidate gene for lysinuric protein intolerance. *Journal of Biological Chemistry*, **1998**, 273, 32437-45	5.4	265
6	The molecular basis of cystinuria: the role of the rBAT gene. *Amino Acids*, **1996**, 11, 225-46	3.5	13
5	Large-Scale Uniform Analysis of Cancer Whole Genomes in Multiple Computing Environments		14
4	The impact of non-additive genetic associations on age-related complex diseases		3
3	Comparative analysis of neutrophil and monocyte epigenomes		2
2	Human pancreatic islet 3D chromatin architecture provides insights into the genetics of type 2 diabetes		7
1	GCAT|Panel, a comprehensive structural variant haplotype map of the Iberian population from high-coverage whole-genome sequencing		1